#7

RAW SEQUENCE LISTING DATE: 09/21/2001
PATENT APPLICATION: US/09/848,035 TIME: 18:04:35

Input Set : A:\SEQUENCE LISTING.TXT
Output Set: N:\CRF3\09212001\I848035.raw


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 4 <110> APPLICANT: Bertin, John
 6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES
THEREOF
 8 <130> FILE REFERENCE: 07334-268001
10 <140> CURRENT APPLICATION NUMBER: US 09/848,035
11 <141> CURRENT FILING DATE: 2001-05-03
13 <150> PRIOR APPLICATION NUMBER: US 60/201,464
14 <151> PRIOR FILING DATE: 2000-05-03
16 <160> NUMBER OF SEQ ID NOS: 17
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2464
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)...(2463)
29 <400> SEQUENCE: 1
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31 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln
32   1               5                  10                  15
34 ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt       96
35 Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe
36              20                  25                  30
38 ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag      144
39 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu
40          35                  40                  45
42 gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa      192
43 Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu
44      50                  55                  60
46 aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc      240
47 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu
48  65                  70                  75                  80
50 acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag      288
51 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln
52                  85                  90                  95
54 gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg      336
55 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser
56              100                 105                 110
58 gag tta gca aag cca ggt gaa aag gaa gga tgg aga aat tca atg gag      384
59 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu
60          115                 120                 125
62 aaa caa tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac      432
63 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp
64      130                 135                 140
66 aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc      480
67 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe
68 145                 150                 155                 160
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70 ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg      528
71 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu
72                 165                 170                 175
74 cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg      576
75 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met
76             180                 185                 190
78 ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc      624
79 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe
80         195                 200                 205
82 tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca      672
83 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala
84     210                 215                 220
86 gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc      720
87 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser
88 225                 230                 235                 240
90 atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat      768
91 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp
92                 245                 250                 255
94 gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac      816
95 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp
96             260                 265                 270
98 tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag      864
99 Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys
100         275                 280                 285
102 agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg      912
103 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg
104     290                 295                 300
106 gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg      960
107 Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg
108 305                 310                 315                 320
110 gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac     1008
111 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His
112                 325                 330                 335
114 ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc     1056
115 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser
116             340                 345                 350
118 aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att     1104
119 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile
120         355                 360                 365
122 gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg     1152
123 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro
124     370                 375                 380
126 gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct     1200
127 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro
128 385                 390                 395                 400
130 cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag     1248
131 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu
132                 405                 410                 415
134 gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg     1296
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135 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
136             420                 425                 430
138 gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac tcc     1344
139 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
140         435                 440                 445
142 ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac gcc     1392
143 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala
144     450                 455                 460
146 ctg gag aag gag gag gag gag gac agg gac ggc cac gcc tgg gac att     1440
147 Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile
148 465                 470                 475                 480
150 ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac ccc     1488
151 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro
152                 485                 490                 495
154 gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag aag     1536
155 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys
156             500                 505                 510
158 aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg gac     1584
159 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp
160         515                 520                 525
162 atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat aag     1632
163 Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys
164     530                 535                 540
166 ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat gag     1680
167 Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu
168 545                 550                 555                 560
170 tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag gaa     1728
171 Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu
172                 565                 570                 575
174 att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc ttc     1776
175 Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe
176             580                 585                 590
178 agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta gca     1824
179 Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala
180         595                 600                 605
182 aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att gaa     1872
183 Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu
184     610                 615                 620
186 ttt gaa agc tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc     1920
187 Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser
188 625                 630                 635                 640
190 ttc ctg agt gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt     1968
191 Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg
192                 645                 650                 655
194 agc acc tgt cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac     2016
195 Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp
196             660                 665                 670
198 acc gcg tac cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc     2064
199 Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu
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200         675                 680                 685
202 acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg     2112
203 Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met
204     690                 695                 700
206 ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac     2160
207 Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr
208 705                 710                 715                 720
210 ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc     2208
211 Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe
212                 725                 730                 735
214 ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca     2256
215 Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser
216             740                 745                 750
218 gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg     2304
219 Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met
220         755                 760                 765
222 aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt     2352
223 Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg
224     770                 775                 780
226 ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc     2400
227 Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser
228 785                 790                 795                 800
230 aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca     2448
231 Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr
232                 805                 810                 815
234 ggg gtg aag ttt ctg t                                           2464
235 Gly Val Lys Phe Leu
236             820
238 <210> SEQ ID NO: 2
239 <211> LENGTH: 821
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 2
244 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln
245   1               5                  10                  15
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247              20                  25                  30
248 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu
249          35                  40                  45
250 Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu
251      50                  55                  60
252 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu
253  65                  70                  75                  80
254 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln
255                  85                  90                  95
256 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser
257             100                 105                 110
258 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu
259         115                 120                 125
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260 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp
261     130                 135                 140
262 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe
263 145                 150                 155                 160
264 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu
265                 165                 170                 175
266 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met
267             180                 185                 190
268 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe
269         195                 200                 205
270 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala
271     210                 215                 220
272 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser
273 225                 230                 235                 240
274 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp
275                 245                 250                 255
276 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp
277             260                 265                 270
278 Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys
279         275                 280                 285
280 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg
281     290                 295                 300
282 Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg
283 305                 310                 315                 320
284 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His
285                 325                 330                 335
286 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser
287             340                 345                 350
288 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile
289         355                 360                 365
290 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro
291     370                 375                 380
292 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro
293 385                 390                 395                 400
294 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu
295                 405                 410                 415
296 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
297             420                 425                 430
298 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
299         435                 440                 445
300 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala
301     450                 455                 460
302 Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile
303 465                 470                 475                 480
304 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro
305                 485                 490                 495
306 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys
307             500                 505                 510
308 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp
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VERIFICATION SUMMARY DATE: 09/21/2001
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